

## BLAST

# Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

### Protein Sequence (21 letters)

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

|cl|55601

|cl|55601

#### Description

None

#### Molecule type

amino acid

#### Query Length

21

#### Database Name

nr

#### Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

#### Program

BLASTP 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Related Structures](#) [Multiple alignment](#) **NEW**

### Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hittlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

### Database

Posted date	Dec 10, 2009 5:41 PM
Number of letters	3,463,213,929
Number of sequences	10,157,076

Entrez query none

**Karlin-Altschul statistics**

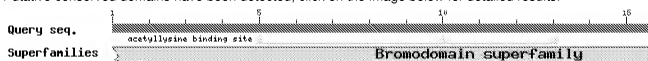
Params	Ungapped	Gapped
Lambda	0.332117	0.294
K	0.27808	0.11
H	1.83624	0.61

**Results Statistics**

Length adjustment	11
Effective length of query	10
Effective length of database	3351486093
Effective search space	33514860930
Effective search space used	33514860930

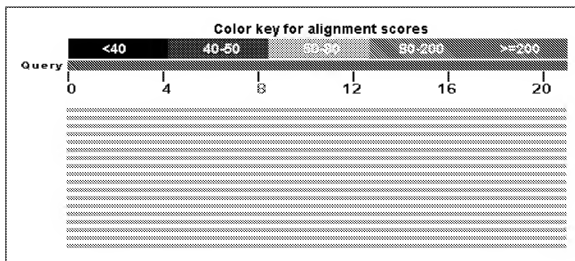
[Graphic Summary](#)[Show Conserved Domains](#)

Putative conserved domains have been detected, click on the image below for detailed results.

**Distribution of 104 Blast Hits on the Query Sequence**

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[illegible]



## Descriptions

E	Sequences producing significant alignments:	Score	
		(Bits)	Value
	<a href="#">pdb136031A</a> Chain A, Crystal Structure Of The Bromodomain Of H...	69.8	3e-11
	<a href="#">ref1XP_002154393.1</a> PREDICTED: p300/CBP-associated factor [Ta...	69.8	3e-11
	<a href="#">ref1XP_001493774.2</a> PREDICTED: p300/CBP-associated factor [Eq...	69.8	3e-11
	<a href="#">ref1XP_001508356.1</a> PREDICTED: similar to PCAF [Ornithorhynch...	69.8	3e-11
	<a href="#">gb1EEL82053.1</a> p300/CBP-associated factor, isoform CRA_b [Rat...	69.8	3e-11
	<a href="#">gb1EEL92852.1</a> p300/CBP-associated factor, isoform CRA_a [Rat...	69.8	3e-11
	<a href="#">gb1EEL23666.1</a> p300/CBP-associated factor, isoform CRA_b [Mus...	69.8	3e-11
	<a href="#">gb1EEL23665.1</a> p300/CBP-associated factor, isoform CRA_a [Mus...	69.8	3e-11
	<a href="#">ref1XP_001380514.1</a> PREDICTED: similar to p300/CBP-associated...	69.8	3e-11
	<a href="#">ref1XP_013744.3</a> PREDICTED: p300/CBP-associated factor [Bos t...	69.8	3e-11
	<a href="#">gb1EAM54305.1</a> p300/CBP-associated factor, isoform CRA_a [Hom...	69.8	3e-11
	<a href="#">gb1EAM54306.1</a> p300/CBP-associated factor, isoform CRA_b [Hom...	69.8	3e-11
	<a href="#">ref1XP_426091.2</a> PREDICTED: similar to PCAF [Gallus gallus]	69.8	3e-11
	<a href="#">ref1XP_016321.2</a> PREDICTED: p300/CBP-associated factor [Pan t...	69.8	3e-11
	<a href="#">ref1XP_001066807.1</a> PREDICTED: similar to p300/CBP-associated...	69.8	3e-11
	<a href="#">gb1EAM59138.1</a> PCAF [Gallus gallus]	69.8	3e-11
	<a href="#">gb1AAC50899.2</a> p300/CBP-associated factor [Homo sapiens]	69.8	3e-11
	<a href="#">gb1AAM70495.1</a> <a href="#">AF254442.1</a> PCAF acetyltransferase [Mus musculus]	69.8	3e-11
	<a href="#">ref1XP_034249.2</a> PREDICTED: similar to p300/CBP-associated fa...	69.8	3e-11
	<a href="#">ref1XP_064089.2</a> K(lysine) acetyltransferase 2B [Mus musculus...	69.8	3e-11
	<a href="#">ref1NP_002875.2</a> K(lysine) acetyltransferase 2B [Homo sapiens...	69.8	3e-11
	<a href="#">gb1EAM23656.1</a> unnamed protein product [Mus musculus]	69.8	3e-11
	<a href="#">pdb1N721A</a> Chain A, Structure And Ligand Of A Histone Acetyl...	69.8	3e-11
	<a href="#">ref1NP_061819425.1</a> K(lysine) acetyltransferase 2B [Rattus no...	66.0	5e-10
	<a href="#">gb1EOL05222.1</a> MCG4405 [Mus musculus]	65.5	6e-10
	<a href="#">ref1XP_011230.1</a> PREDICTED: similar to P300/CBP-associated fa...	65.5	6e-10
	<a href="#">ref1XP_294106.1</a> PREDICTED: similar to P300/CBP-associated fa...	65.5	6e-10
	<a href="#">ref1NP_001038499.1</a> K(lysine) acetyltransferase 2B [Danio rerio...	59.6	4e-08
	<a href="#">emb1CAF99403.1</a> unnamed protein product [Tetraodon nigroviridis]	59.6	4e-08
	<a href="#">pdb129751A</a> Chain A, Crystal Structure Of The Bromodomain Of H...	54.9	1e-06
	<a href="#">ref1XP_001425139.2</a> PREDICTED: similar to GCN5 general contro...	54.9	1e-06
	<a href="#">ref1XP_001922732.1</a> PREDICTED: im:7156024 [Danio rerio]	54.9	1e-06
	<a href="#">gb1EEL02549.1</a> GCN5 general control of amino acid synthesis-1...	54.9	1e-06
	<a href="#">gb1EEL02553.1</a> GCN5 general control of amino acid synthesis-1...	54.9	1e-06
	<a href="#">gb1EAM60301.1</a> GCN5 general control of amino-acid synthesis 5...	54.9	1e-06
	<a href="#">gb1EAM60302.1</a> GCN5 general control of amino-acid synthesis 5...	54.9	1e-06
	<a href="#">ref1XP_011509.2</a> PREDICTED: GCN5 general control of amino-aci...	54.9	1e-06
	<a href="#">ref1XP_001166739.1</a> PREDICTED: GCN5 general control of amino-...	54.9	1e-06
	<a href="#">ref1NP_001100520.1</a> general control of amino acid synthesis 5...	54.9	1e-06
	<a href="#">ref1XP_001074222.1</a> PREDICTED: similar to GCN5 general contro...	54.9	1e-06
	<a href="#">gb1AAR03354.1</a> general control of amino-acid synthesis 5-like...	54.9	1e-06
	<a href="#">gb1AAR03352.1</a> Kat2a protein [Mus musculus]	54.9	1e-06
	<a href="#">pdb1T5581A</a> Chain A, Nmr Solution Structure Of The Bromodomain...	54.9	1e-06
	<a href="#">gb1AAC50899.1</a> GCN5 [Homo sapiens]	54.9	1e-06

ref XP_000469.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_000469.1	PREDICTED: similar to General control of ami...	54.9	1e-06
ref XP_000469.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_000469.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_000469.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_000469.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_000469.1	hGCN5=transcriptional adaptor [human, testis, ...	54.9	1e-06
ref NP_066564.2	general control of amino acid synthesis 5-li...	54.9	1e-06
gb BAE26296.1	unnamed protein product [Mus musculus]	54.9	1e-06
gb BAE26296.1	unnamed protein product [Mus musculus]	54.9	1e-06
gb BAE26297.1	unnamed protein product [Mus musculus]	54.9	1e-06
ref NP_066564.2	general control of amino acid synthesis 5-li...	54.9	1e-06
ref NP_001030299.1	general control of amino acid synthesis 5...	54.9	1e-06
sp Q2J8D2.1 KAT5_MOUSE	RecName: Full=Histone acetyltransferase...	54.9	1e-06
gb AA039769.1	hGCN5 [Homo sapiens]	54.9	1e-06
ref XP_001015022.1	PREDICTED: similar to GCN5 general contro...	54.5	1e-06
ref XP_001015022.1	PREDICTED: GCN5 general control of amino...	52.8	4e-06
emb CAC09299.1	unnamed protein product [Tetraodon nigroviridis]	52.8	4e-06
ref NP_099566.1	general control of amino acid synthesis 5-li...	52.8	4e-06
ref XP_001015022.1	PREDICTED: similar to K(lysine) acetyltra...	51.1	1e-05
gb E010157.1	hypothetical protein TcasGA2_TC012345 [Triboli...	49.6	8e-05
ref XP_002427489.1	fetal alzheimer antigen, falz, putative [...	48.6	8e-05
ref XP_001015022.1	PREDICTED: similar to fetal alzheimer ant...	48.6	8e-05
ref NP_001084589.1	GH14490 [Drosophila grimshawi] >gb EDV978...	46.0	5e-04
ref XP_001015022.1	PREDICTED: similar to fetal alzheimer ant...	44.8	0.001
ref XP_001015022.1	PREDICTED: similar to Enhancer of bithorax C...	44.6	0.001
ref XP_002093980.1	GE21036 [Drosophila yakuba] >gb EDW92692...	44.3	0.002
ref XP_001015022.1	GG14675 [Drosophila erecta] >gb EDV50020...	44.2	0.002
gb A010154.1 AF417921.1	nucleosome remodeling factor large s...	43.2	0.002
ref NP_001015022.1	enhancer of bithorax, isoform B [Drosophila ...	44.3	0.002
ref NP_001015022.1	enhancer of bithorax, isoform A [Drosophila ...	44.3	0.002
ref XP_002117619.1	predicted protein [Trichoplax adhaerens] ...	43.9	0.002
ref XP_002117619.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_002117619.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_002117619.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_002117619.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_001015022.1	GA16840 [Drosophila pseudoobscura pseudo...	43.5	0.003
ref XP_002026664.1	GL16133 [Drosophila persimilis] >gb EDW33...	43.5	0.003
ref XP_001015022.1	GF24755 [Drosophila ananassae] >gb EDV389...	43.5	0.003
ref XP_002026664.1	GK17657 [Drosophila willistoni] >gb EDW73...	43.1	0.004
ref XP_002026664.1	GJ16047 [Drosophila virilis] >gb EDW57119...	43.1	0.004
ref XP_001015022.1	GH15750 [Drosophila grimshawi] >gb EDV955...	43.1	0.004
ref XP_002026664.1	histone acetyltransferase GCN5 [Ajellomyces ...	42.6	0.005
ref XP_001015022.1	AGAP006133-PA [Anopheles gambiae str. PEST] ...	42.6	0.005
ref XP_002026664.1	histone acetyltransferase (Gcn5), putativ...	42.2	0.007
ref XP_001015022.1	hypothetical protein An01g08160 [Aspergill...	42.2	0.007
ref XP_001015022.1	histone acetyltransferase (Gcn5), putativ...	42.2	0.007
ref XP_001015022.1	histone acetyltransferase (Gcn5), putativ...	42.2	0.007

ref XP_001412347.1	histone acetyltransferase GCN5 [Aspergill...	44.2	0.007
ref XP_001412347.1	hypothetical protein [Aspergillus oryzae ...	42.2	0.007
ref XP_001412347.1	histone acetyltransferase (Gcn5) [Aspergillu...	42.2	0.007
gb EPP24293.1	histone acetyltransferase GCN5, putative [Cocc...	41.8	0.009
ref XP_002541068.1	histone acetyltransferase GCN5 [Uncinocar...	41.8	0.009
gb EEM45435.1	histone acetyltransferase GCN5 [Paracoccidioid...	41.8	0.009
gb EEM45435.1	histone acetyltransferase GCN5 [Paracoccidioid...	41.8	0.009
gb EEM45435.1	histone acetyltransferase GCN5 [Paracoccidioid...	41.8	0.009

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>pdb|3GG3|A  Chain A, Crystal Structure Of The Bromodomain Of Human Pcaf  
 pdb|3GG3|B  Chain B, Crystal Structure Of The Bromodomain Of Human Pcaf  
 Length=119

Score = 69.8 bits (157), Expect = 3e-11  
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEYEVIRSPM 21  
 FMEPVKRTAPGYEYEVIR PM  
 Sbjct 36 FMEPVKRTAPGYEYEVIRFPM 56

>ref|XP\_002194393.1|  PREDICTED: p300/CBP-associated factor [Taeniopygia gutt  
 Length=742

GENE ID: 100227387 LOC100227387 | p300/CBP-associated factor  
 [Taeniopygia guttata]

Score = 69.8 bits (157), Expect = 3e-11  
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTAPGYEYEVIRSPM 21  
 FMEPVKRTAPGYEYEVIR PM  
 Sbjct 658 FMEPVKRTAPGYEYEVIRFPM 678

>ref|XP\_001493774.2|  PREDICTED: p300/CBP-associated factor [Equus caballus]  
 Length=784

GENE ID: 100061976 KAT2B | K(lysine) acetyltransferase 2B [Equus caballus]

Score = 69.8 bits (157), Expect = 3e-11  
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTAPGYEYEVIRSPM 21  
 FMEPVKRTAPGYEYEVIR PM  
 Sbjct 700 FMEPVKRTAPGYEYEVIRFPM 720

>ref|XP\_001508358.1|  PREDICTED: similar to PCAF [Ornithorhynchus anatinus]  
 Length=817

GENE ID: 100077074 LOC100077074 | similar to PCAF [Ornithorhynchus anatinus]

Score = 69.8 bits (157), Expect = 3e-11  
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTAPGYEYEVIRSPM 21  
 FMEPVKRTAPGYEYEVIR PM  
 Sbjct 733 FMEPVKRTAPGYEYEVIRFPM 753

>gb|EDL82853.1|  p300/CBP-associated factor, isoform CRA\_b [Rattus norvegicus]  
 Length=704

GENE ID: 301164 Pcaf | p300/CBP-associated factor [Rattus norvegicus]  
 (10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM  
Sbjct 620 FMEPVKRTAPGYEIVIRFPM 640

>**gb|EDL82852.1|**  p300/CBP-associated factor, isoform CRA\_a [Rattus norvegicus]  
Length=731

**GENE ID: 301164 Pcaf** | p300/CBP-associated factor [Rattus norvegicus]  
(10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM  
Sbjct 647 FMEPVKRTAPGYEIVIRFPM 667

>**gb|EDL23666.1|**  p300/CBP-associated factor, isoform CRA\_b [Mus musculus]  
Length=706

**GENE ID: 18519 Kat2b** | K(lysine) acetyltransferase 2B [Mus musculus]  
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM  
Sbjct 622 FMEPVKRTAPGYEIVIRFPM 642

>**gb|EDL23665.1|**  p300/CBP-associated factor, isoform CRA\_a [Mus musculus]  
Length=746

**GENE ID: 18519 Kat2b** | K(lysine) acetyltransferase 2B [Mus musculus]  
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM  
Sbjct 662 FMEPVKRTAPGYEIVIRFPM 682

>**ref|XP\_001380514.1|**  PREDICTED: similar to p300/CBP-associated factor, [Mono domestica]  
Length=966

**GENE ID: 100031193 LOC100031193** | similar to p300/CBP-associated factor  
[Monodelphis domestica]

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM  
Sbjct 882 FMEPVKRTAPGYEIVIRFPM 902

>**ref|XP\_613744.3|**  PREDICTED: p300/CBP-associated factor [Bos taurus]  
Length=826

**GENE ID: 407215 KAT2B** | K(lysine) acetyltransferase 2B [Bos taurus]

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM

Sbjct 742 FMEPVKRTAPGYEIVIRFPM 762

>gb|EAW64305.1| p300/CBP-associated factor, isoform CRA\_a [Homo sapiens]  
Length=825

GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]  
(Over 100 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM  
Sbjct 741 FMEPVKRTAPGYEIVIRFPM 761

>gb|EAW64306.1| p300/CBP-associated factor, isoform CRA\_b [Homo sapiens]  
Length=768

GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]  
(Over 100 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM  
Sbjct 741 FMEPVKRTAPGYEIVIRFPM 761

>ref|XP\_426001.2| PREDICTED: similar to PCAF [Gallus gallus]  
Length=753

GENE ID: 428441 PCAF | p300/CBP-associated factor [Gallus gallus]  
(10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM  
Sbjct 669 FMEPVKRTAPGYEIVIRFPM 689

>ref|XP\_516321.2| PREDICTED: p300/CBP-associated factor [Pan troglodytes]  
Length=806

GENE ID: 460219 KAT2B | K(lysine) acetyltransferase 2B [Pan troglodytes]

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM  
Sbjct 722 FMEPVKRTAPGYEIVIRFPM 742

>ref|XP\_001086807.1| PREDICTED: similar to p300/CBP-associated factor [Macaca mulatta]  
Length=858

GENE ID: 698283 LOC698283 | similar to p300/CBP-associated factor  
[Macaca mulatta]

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVKRTAPGYEIVIR PM  
Sbjct 774 FMEPVKRTAPGYEIVIRFPM 794

>dbj|BAB59138.1| PCAF [Gallus gallus]  
Length=760



**GENE ID: 428441 PCAF** | p300/CBP-associated factor [Gallus gallus]  
(10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query	1	FMEPVKRTAPGYEIVIRSPM	21
		FMEPVKRTAPGYEIVIR PM	
Sbjct	676	FMEPVKRTAPGYEIVIRFPM	696

>**gb|AAC50890.2|G** p300/CBP-associated factor [Homo sapiens]  
Length=832

**GENE ID: 8850 KAT2B** | K(lysine) acetyltransferase 2B [Homo sapiens]  
(Over 100 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query	1	FMEPVKRTAPGYEIVIRSPM	21
		FMEPVKRTAPGYEIVIR PM	
Sbjct	748	FMEPVKRTAPGYEIVIRFPM	768

>**gb|AAF70498.1|AF254442\_1G** PCAF acetyltransferase [Mus musculus]  
Length=813

**GENE ID: 18519 Kat2b** | K(lysine) acetyltransferase 2B [Mus musculus]  
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query	1	FMEPVKRTAPGYEIVIRSPM	21
		FMEPVKRTAPGYEIVIR PM	
Sbjct	729	FMEPVKRTAPGYEIVIRFPM	749

>**ref|XP\_534249.2|UG** PREDICTED: similar to p300/CBP-associated factor [Canis fa  
Length=760

**GENE ID: 477052 KAT2B** | K(lysine) acetyltransferase 2B [Canis lupus familiaris]  
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query	1	FMEPVKRTAPGYEIVIRSPM	21
		FMEPVKRTAPGYEIVIR PM	
Sbjct	676	FMEPVKRTAPGYEIVIRFPM	696

>**ref|NP\_064389.2|UG** K(lysine) acetyltransferase 2B [Mus musculus]  
**sp|Q9JHD1.2|KAT2B\_MOUSEG** RecName: Full=Histone acetyltransferase KAT2B; AltName: acetyltransferase 2B; AltName: Full=Histone acetyltransferase PCAF; Short=Histone acetylase PCAF; AltName: Full=P300/CBP-associated factor; Short=P/CAF





**gb|AAH82581.1|G** K(lysine) acetyltransferase 2B [Mus musculus]  
**gb|EDL23667.1|G** p300/CBP-associated factor, isoform CRA\_c [Mus musculus]  
**gb|AAI45897.1|G** K(lysine) acetyltransferase 2B [Mus musculus]  
**gb|AAI38196.1|G** K(lysine) acetyltransferase 2B [Mus musculus]  
Length=813

**GENE ID: 18519 Kat2b** | K(lysine) acetyltransferase 2B [Mus musculus]  
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11  
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query	1	FMEPVKRTAPGYEIVIRSPM	21
		FMEPVKRTAPGYEIVIR PM	
Sbjct	729	FMEPVKRTAPGYEIVIRFPM	749


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>ref|NP_003875.3|  K(lysine) acetyltransferase 2B [Homo sapiens]
  sp|Q92831.3|KAT2B_HUMAN  RecName: Full=Histone acetyltransferase KAT2B; AltName acetyltransferase 2B; AltName: Full=Histone acetyltransferase PCAF; Short=Histone acetylase PCAF; AltName: Full=P300/CBP-associated factor; Short=P/CAF
  gb|AAH60823.1|  K(lysine) acetyltransferase 2B [Homo sapiens]
  gb|AAH70075.1|  K(lysine) acetyltransferase 2B [Homo sapiens]
  dbj|BAI45566.1| K(lysine) acetyltransferase 2B [synthetic construct]
  Length=832

  GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]
  (Over 100 PubMed links)

  Score = 69.8 bits (157), Expect = 3e-11
  Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)








  Query 1 FMEPVKRTTEAPGYEYEVIRSPM 21
          FMEPVKRTTEAPGYEYEVIR PM
  Sbjet 748 FMEPVKRTTEAPGYEYEVIRFPM 768

>dbj|BAE33658.1|  unnamed protein product [Mus musculus]
  Length=813

  GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
  (Over 10 PubMed links)



  Score = 69.8 bits (157), Expect = 3e-11
  Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

  Query 1 FMEPVKRTTEAPGYEYEVIRSPM 21
          FMEPVKRTTEAPGYEYEVIR PM
  Sbjet 729 FMEPVKRTTEAPGYEYEVIRFPM 749

>pdb|1N72|A  Chain A, Structure And Ligand Of A Histone Acetyltransferase Bromodomain
  bromodomain
  pdb|1JM4|B  Chain B, Nmr Structure Of PCAF BROMODOMAIN IN COMPLEX WITH HIV-1 Tat Peptide
  Tat Peptide
  pdb|1WUG|A  Chain A, Complex Structure Of Pcaf Bromodomain With Small Chemic Ligand Np1
  Ligand Np1
  pdb|1WUM|A  Chain A, Complex Structure Of Pcaf Bromodomain With Small Chemic Ligand Np2
  Ligand Np2
  pdb|1ZS5|A  Chain A, Structure-Based Evaluation Of Selective And Non-Selecti Small Molecules That Block Hiv-1 Tat And Pcaf Association
  Small Molecules That Block Hiv-1 Tat And Pcaf Association
  pdb|2RNW|A  Chain A, The Structural Basis For Site-Specific Lysine-Acetylate Histone Recognition By The Bromodomains Of The Human Transcriptional Co-Activators Pcaf And Cbp
  Co-Activators Pcaf And Cbp
  pdb|2RNX|A  Chain A, The Structural Basis For Site-Specific Lysine-Acetylate Histone Recognition By The Bromodomains Of The Human Transcriptional Co-Activators Pcaf And Cbp
  Co-Activators Pcaf And Cbp
  Length=118

  Score = 69.8 bits (157), Expect = 3e-11
  Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

  Query 1 FMEPVKRTTEAPGYEYEVIRSPM 21
          FMEPVKRTTEAPGYEYEVIR PM
  Sbjet 34 FMEPVKRTTEAPGYEYEVIRFPM 54

>ref|NP_001019423.1|  K(lysine) acetyltransferase 2B [Rattus norvegicus]
  gb|AAH92639.1|  P300/CBP-associated factor [Rattus norvegicus]
  Length=84

  GENE ID: 301164 Pcaf | p300/CBP-associated factor [Rattus norvegicus]
  (10 or fewer PubMed links)

  Score = 66.0 bits (148), Expect = 5e-10

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Identities = 19/20 (95%), Positives = 19/20 (95%), Gaps = 0/20 (0%)

Query 2 MEPVKRTEAPGYEIVIRSPM 21  
MEPVKRTAPGYEIVIR PM  
Sbjct 1 MEPVKRTEAPGYEIVIRFPM 20

>gb|EDL05223.1| mCG4405 [Mus musculus]  
Length=813

Score = 65.5 bits (147), Expect = 6e-10  
Identities = 19/21 (90%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTAPGYEIVIRSPM 21  
F+EPVKRTAPGYEIVIR PM  
Sbjct 729 FLEPVKRTAPGYEIVIRFPM 749

>ref|XP\_911230.1|  PREDICTED: similar to P300/CBP-associated factor [Mus musculus]  
Length=829

GENE ID: 330129 Gm5109 | predicted gene 5109 [Mus musculus]

Score = 65.5 bits (147), Expect = 6e-10  
Identities = 19/21 (90%), Positives = 20/21 (95%), Gaps = 0/21 (0%)




Query 1 FMEPVKRTAPGYEIVIRSPM 21  
F+EPVKRTAPGYEIVIR PM  
Sbjct 745 FLEPVKRTAPGYEIVIRFPM 765

>ref|XP\_284106.1|  PREDICTED: similar to P300/CBP-associated factor [Mus musculus]  
Length=829

GENE ID: 330129 Gm5109 | predicted gene 5109 [Mus musculus]

Score = 65.5 bits (147), Expect = 6e-10  
Identities = 19/21 (90%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEIVIRSPM 21  
F+EPVKRTAPGYEIVIR PM  
Sbjct 745 FLEPVKRTAPGYEIVIRFPM 765

>ref|NP\_001038499.1|  K(lysine) acetyltransferase 2B [Danio rerio]  
|CAK04378.1|  novel protein similar to vertebrate p300/CBP-associated factor (PCAF) [Danio rerio]  
Length=796

GENE ID: 563942 kat2b | K(lysine) acetyltransferase 2B [Danio rerio]  
(10 or fewer PubMed links)


Score = 59.6 bits (133), Expect = 4e-08  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVK+ EAPGY+VIR PM  
Sbjct 712 FMEPVKNEAPGY+QVIRFPM 732

>emb|CAF99403.1| unnamed protein product [Tetraodon nigroviridis]  
Length=701

Score = 59.6 bits (133), Expect = 4e-08  
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTAPGYEIVIRSPM 21  
FMEPVK+TEAPGY+ IR PM  
Sbjct 617 FMEPVKTEAPGY+QAIRFPM 637

>pdb|3D7C|A  Chain A, Crystal Structure Of The Bromodomain Of Human Gcn5,  
The General Control Of Amino-Acid Synthesis Protein 5-Like 2

>pdb|3D7C|B  Chain B, Crystal Structure Of The Bromodomain Of Human Gcn5,  
The General Control Of Amino-Acid Synthesis Protein 5-Like 2

Length=112

Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEYEVIRSP 20  
 FMEPVK++EAP YEEVIR P  
 Sbjct 28 FMEPVKKSEAPDYEEVIRFP 47

>**ref|XP\_001495139.2|** **UG** PREDICTED: similar to GCN5 general control of amino-acid synthesis 5-like 2 [Equus caballus]  
 Length=836

**GENE ID: 100053057 LOC100053057** | similar to GCN5 general control of amino-acid synthesis 5-like 2 [Equus caballus]

Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEYEVIRSP 20  
 FMEPVK++EAP YEEVIR P  
 Sbjct 752 FMEPVKKSEAPDYEEVIRFP 771

>**ref|XP\_001922732.1|** **UG** PREDICTED: im:7156024 [Danio rerio]  
 Length=795

**GENE ID: 555517 kat2a** | K(lysine) acetyltransferase 2A [Danio rerio]  
 (10 or fewer PubMed links)

Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEYEVIRSP 20  
 FMEPVK++EAP YEEVIR P  
 Sbjct 711 FMEPVKKSEAPDYEEVIRFP 730

>**gb|EDL02540.1|** **G** GCN5 general control of amino acid synthesis-like 2 (yeast), isoform CRA\_c [Mus musculus]  
 Length=481

**GENE ID: 14534 Kat2a** | K(lysine) acetyltransferase 2A [Mus musculus]  
 (Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEYEVIRSP 20  
 FMEPVK++EAP YEEVIR P  
 Sbjct 397 FMEPVKKSEAPDYEEVIRFP 416

>**gb|EDL02538.1|** **G** GCN5 general control of amino acid synthesis-like 2 (yeast), isoform CRA\_a [Mus musculus]  
 Length=845

**GENE ID: 14534 Kat2a** | K(lysine) acetyltransferase 2A [Mus musculus]  
 (Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEYEVIRSP 20  
 FMEPVK++EAP YEEVIR P  
 Sbjct 761 FMEPVKKSEAPDYEEVIRFP 780

>**gb|EAW60801.1|** **G** GCN5 general control of amino-acid synthesis 5-like 2 (yeast), isoform CRA\_a [Homo sapiens]  
 Length=477

**GENE ID: 2648 KAT2A** | K(lysine) acetyltransferase 2A [Homo sapiens]  
 (Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAEAPGYEVIRSP 20  
FMEPVK++EAP YVEVIR P  
Sbjct 393 FMEPVKKSEAPDYEVIRFP 412

>**gb|EAW60802.1|** **G** GCN5 general control of amino-acid synthesis 5-like 2 (yeast), isoform CRA\_b [Homo sapiens]  
Length=838

**GENE ID: 2648 KAT2A** | K(lysine) acetyltransferase 2A [Homo sapiens]  
(Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAEAPGYEVIRSP 20  
FMEPVK++EAP YVEVIR P  
Sbjct 754 FMEPVKKSEAPDYEVIRFP 773

>**ref|XP\_511500.2|** **UG** PREDICTED: GCN5 general control of amino-acid synthesis 5-2 isoform 2 [Pan troglodytes]  
Length=837

**GENE ID: 454677 KAT2A** | K(lysine) acetyltransferase 2A [Pan troglodytes]

Score = 54.9 bits (122), Expect = 1e-06  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAEAPGYEVIRSP 20  
FMEPVK++EAP YVEVIR P  
Sbjct 753 FMEPVKKSEAPDYEVIRFP 772

>**ref|XP\_001166738.1|** **UG** PREDICTED: GCN5 general control of amino-acid synthesis 2 isoform 1 [Pan troglodytes]  
Length=852

**GENE ID: 454677 KAT2A** | K(lysine) acetyltransferase 2A [Pan troglodytes]

Score = 54.9 bits (122), Expect = 1e-06  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAEAPGYEVIRSP 20  
FMEPVK++EAP YVEVIR P  
Sbjct 768 FMEPVKKSEAPDYEVIRFP 787

>**ref|NP\_001100520.1|** **G** general control of amino acid synthesis 5-like 2 [Rattus  
**gb|EDM06059.1|** **G** GCN5 general control of amino acid synthesis-like 2 (yeast) (p  
[Rattus norvegicus]  
Length=832

**GENE ID: 303539 Gcn512** | GCN5 general control of amino acid synthesis-like 2 (yeast) [Rattus norvegicus]

Score = 54.9 bits (122), Expect = 1e-06  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAEAPGYEVIRSP 20  
FMEPVK++EAP YVEVIR P  
Sbjct 748 FMEPVKKSEAPDYEVIRFP 767

>**ref|XP\_001094333.1|** **UG** PREDICTED: similar to GCN5 general control of amino-acid 5-like 2 [Macaca mulatta]  
Length=608

**GENE ID: 706004 LOC706004** | similar to GCN5 general control of amino-acid synthesis 5-like 2 [Macaca mulatta]

Score = 54.9 bits (122), Expect = 1e-06


Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTTEAPGYEYEVIRSP 20  
FMEPVK++EAP YYEYEVIR P  
Sbjct 524 FMEPVKKSEAPDYEYEVIRFP 543

>**gb|AAR03834.1|** general control of amino-acid synthesis 5-like 2 [Sus scrofa]  
Length=117

Score = 54.9 bits (122), Expect = 1e-06  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


Query 1 FMEPVKRTTEAPGYEYEVIRSP 20  
FMEPVK++EAP YYEYEVIR P  
Sbjct 33 FMEPVKKSEAPDYEYEVIRFP 52

>**gb|AAH03983.1|**  Kat2a protein [Mus musculus]  
Length=116

**GENE ID: 14534 Kat2a** | K(lysine) acetyltransferase 2A [Mus musculus]  
(Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTTEAPGYEYEVIRSP 20  
FMEPVK++EAP YYEYEVIR P  
Sbjct 32 FMEPVKKSEAPDYEYEVIRFP 51

>**pdb|1F68|A**  Chain A, Nmr Solution Structure Of The Bromodomain From Human  
Gcn5  
Length=103

Score = 54.9 bits (122), Expect = 1e-06  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


Query 1 FMEPVKRTTEAPGYEYEVIRSP 20  
FMEPVK++EAP YYEYEVIR P  
Sbjct 24 FMEPVKKSEAPDYEYEVIRFP 43

>**gb|AAC50641.1|**  GCN5 [Homo sapiens]  
Length=476

**GENE ID: 2648 KAT2A** | K(lysine) acetyltransferase 2A [Homo sapiens]  
(Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


Query 1 FMEPVKRTTEAPGYEYEVIRSP 20  
FMEPVK++EAP YYEYEVIR P  
Sbjct 392 FMEPVKKSEAPDYEYEVIRFP 411

>**ref|XP\_860469.1|**  PREDICTED: similar to GCN5 general control of amino-acid s  
5-like 2 isoform 7 [Canis familiaris]  
Length=831

**GENE ID: 490971 KAT2A** | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06  
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTTEAPGYEYEVIRSP 20  
FMEPVK++EAP YYEYEVIR P  
Sbjct 747 FMEPVKKSEAPDYEYEVIRFP 766

>**ref|XP\_860436.1|**  PREDICTED: similar to General control of amino acid synthe  
protein 5-like 2 (Histone acetyltransferase GCN5) (mmGCN5)  
isoform 6 [Canis familiaris]  
Length=843

**GENE ID: 490971 KAT2A** | K(lysine) acetyltransferase 2A [Canis lupus familiaris]  
 Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEVIRSP 20  
 FMEPVK++EAP YYEVIR P  
 Sbjct 759 FMEPVKKSEAPDYEVIRFP 778

>**ref|XP\_860364.1|** **UG** PREDICTED: similar to GCN5 general control of amino-acid s  
 5-like 2 isoform 4 [Canis familiaris]  
 Length=584

**GENE ID: 490971 KAT2A** | K(lysine) acetyltransferase 2A [Canis lupus familiaris]  
 Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEVIRSP 20  
 FMEPVK++EAP YYEVIR P  
 Sbjct 500 FMEPVKKSEAPDYEVIRFP 519

>**ref|XP\_860401.1|** **G** PREDICTED: similar to GCN5 general control of amino-acid syn  
 5-like 2 isoform 5 [Canis familiaris]  
 Length=834

**GENE ID: 490971 KAT2A** | K(lysine) acetyltransferase 2A [Canis lupus familiaris]  
 Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEVIRSP 20  
 FMEPVK++EAP YYEVIR P  
 Sbjct 750 FMEPVKKSEAPDYEVIRFP 769

>**ref|XP\_849978.1|** **UG** PREDICTED: similar to GCN5 general control of amino-acid s  
 5-like 2 isoform 2 [Canis familiaris]  
 Length=844

**GENE ID: 490971 KAT2A** | K(lysine) acetyltransferase 2A [Canis lupus familiaris]  
 Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEVIRSP 20  
 FMEPVK++EAP YYEVIR P  
 Sbjct 760 FMEPVKKSEAPDYEVIRFP 779

>**ref|XP\_548094.2|** **UG** PREDICTED: similar to GCN5 general control of amino-acid s  
 5-like 2 isoform 1 [Canis familiaris]  
 Length=837

**GENE ID: 490971 KAT2A** | K(lysine) acetyltransferase 2A [Canis lupus familiaris]  
 Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEVIRSP 20  
 FMEPVK++EAP YYEVIR P  
 Sbjct 753 FMEPVKKSEAPDYEVIRFP 772

>**gb|AAB50690.1|** hGCN5=transcriptional adaptor [human, testis, Peptide, 427 aa]  
 Length=427

Score = 54.9 bits (122), Expect = 1e-06  
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTAPGYEVIRSP 20  
 FMEPVK++EAP YYEVIR P  
 Sbjct 343 FMEPVKKSEAPDYEVIRFP 362